

10 30 50
-88 GTTGTCTGGGCAGCCAAGTTGGCATATTGGAAGCTTTTCCGGGCTCTGGAGGAGGGT-29

70 90 110
-28 CCCTGCTTCTTCTACAGCCGTTCCGGGCATGGCCTGGCTGGGGCGTCGCTCCACGTCT 31
-8 M A W L G A S L H V W 11

130 150 170
32 GGGGTTGGCTAATGCTCGGCAGCTGCCTCCTGGCCAGAGCCCAGCTGGATTCTGATGGCA 91
12 G W L M L G S C L L A R A Q L D S D G T 31

190 210 230
92 CCATCACTATAGAGGAGCAGATTGTCTTGTGCTGAAAGCGAAAGTACAATGTGAACITCA 151
32 I T I E E Q I V L V L K A K V Q C E L N 51

250 270 290
152 ACATCACAGCTCAACTCCAGGAGGAGAGGTAATTGTTCCCTGAATGGGATGGACTCA 211
52 I T A Q L Q E G E G N C F P E W D G L I 71

310 330 350
212 TTTGTTGGCCAGAGGAACAGTGGGGAAAATATCGGCTGTTCCATGCCCTCCTTATATT 271
72 C W P R G T V G K I S A V P C P Y I Y 91

370 390 410
272 ATGACTTCAACCATAAAGGAGTTGCTTCCGACACGTGAACCCCAATGGAACAATGGGATT 331
92 D F N H K G V A F R H C N P N G T W D F 111

MATCH WITH FIG. 1B

FIG.1A

MATCH WITH FIG. 1A

| | | | | | |
|-----|---|-----|-----|-----|-----|
| 332 | TTATGCACAGCTTAAATAAAACATGGGCCAATTATTTCAGACTGCCCTTCGCTTCTGCAGC | 430 | 450 | 470 | 391 |
| 112 | M H S L N K T W A N Y S D C L R F L Q P | | | | 131 |
| 392 | CAGATATCAGCATAGGAAAGCAAGAAATTCGTGAACGCCTCTATGTAATGTATACCGTTG | 490 | 510 | 530 | 451 |
| 132 | D I S I G K Q E F C E R L Y V M Y T V G | | | | 151 |
| 452 | GCTACTCCATCTCTTTTGGTTCCCTTGGCTGTGGCTATTCTCATCATTTGGTTACTTCAGAC | 550 | 570 | 590 | 511 |
| 152 | Y S I S F G S L A V A I L I I G Y F R R | | | | 171 |
| 512 | GATTGCATTGCAC TAGGA ACTATATCCACATGCAC TTA TTTG TGTCTTTTCATGTGAGAG | 610 | 630 | 650 | 571 |
| 172 | L H C T R N Y I H M H L F V S F M L R A | | | | 191 |
| 572 | CTACAAGCATCTTTGTCAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGG | 670 | 690 | 710 | 631 |
| 192 | T S I F V K D R V V H A H I G V K E L E | | | | 211 |
| 632 | AGTCCCTAATAATGCAGGATGACCCACAAAATTCATTGAGGCAACTTCTGTGGACAAAT | 730 | 750 | 770 | 691 |
| 212 | S L I M Q D D P Q N S I E A T S V D K S | | | | 231 |
| 790 | | 810 | 830 | | |

MATCH WITH FIG. 1C

FIG. 1B

MATCH WITH FIG. 1B

| | | |
|------|---|------|
| 692 | CACAATATATCGGGTGAAGATTGCTGTTGTGATGTTTATTACTTCCTGGCTACAAATT | 751 |
| 232 | Q Y I G C K I A V V M F I Y F L A T N Y | 251 |
| | | |
| 752 | ATTATTGGATCCTGTGGGAAGTCTCTACCTGCATAATCTCATCTTTTGCGCTTCTTTT | 811 |
| 252 | Y W I L V E G L Y L H N L I F V A F F S | 271 |
| | | |
| 812 | CGGACACCAATAACCTGTGGGGCTTCATCTTGATAGGCTGGGGTTTCCAGCAGCATTTG | 871 |
| 272 | D T K Y L W G F I L I G W G F P A A F V | 291 |
| | | |
| 872 | TTGCAGCATGGGCTGTGGCAGCAACTCTGGCTGATGCGAGGTGCTGGGAACCTTAGTG | 931 |
| 292 | A A W A V A R A T L A D A R C W E L S A | 311 |
| | | |
| 932 | CTGGAGACATCAAGTGGATTATCAAGCACCGATCTTAGCAGCTATTGGGCTGAATTTTA | 991 |
| 312 | G D I K W I Y Q A P I L A A I G L N F I | 331 |
| | | |
| 992 | TTCGTCTTCTGAATACGGTTAGAGTTCTAGCTACCAAATCTGGGAGACCAATGCAGTTG | 1051 |
| 332 | L F L N T V R V L A T K I W E T N A V G | 351 |
| | | |
| 1052 | GGCATGACACAAGGAAGCAATACAGGAACTGGCCAAATCGACACTGGTCTGTCCTAG | 1111 |
| 352 | H D T R K Q Y R K L A K S T L V L V L V | 371 |

MATCH WITH FIG. 1D

FIG.1C

| | | | | | |
|------|---|------|------|------|------|
| 1112 | TCITTTGGAGTGCATTACATCGTGTTCGTGTCCTGCCTCACTCCTTCACTGGGCTCGGGT | 1210 | 1230 | 1250 | 1171 |
| 372 | F G V H Y I V F V C L P H S F T G L G W | | | | 391 |
| 1172 | GGGAGATCCGCATGCACCTGTGAGCTCTTCTTCAACTCCTTTCAGGGTTTCTTTGTGICTA | 1270 | 1290 | 1310 | 1231 |
| 392 | E I R M H C E L F F N S F Q G F F V S I | | | | 411 |
| 1232 | TCATCTACTGCTACTGCAATGGAGAGGTTTCAGGCAGAGGTGAAGAAGATGTGGAGTCGGT | 1330 | 1350 | 1370 | 1291 |
| 412 | I Y C Y C N G E V Q A E V K K M W S R W | | | | 431 |
| 1292 | GGAATCTCTCCGTGGACTGGAAAGGACACCGCCCATGTGGCAGCCGCAGATGCGGCTCAG | 1390 | 1410 | 1430 | 1351 |
| 432 | N L S V D W K R T P P C G S R R C G S V | | | | 451 |
| 1352 | TGCTCACCACCGTGACGCACAGCACCGAGCCAGTCACAGGTGGCGGCAGCACACGCAT | 1450 | 1470 | 1490 | 1411 |
| 452 | L T T V T H S T S S Q S Q V A A A H A W | | | | 471 |
| 1412 | GGTGCTTATCTCTGGCAAAGCTGCCAAGATCGCCAGCAGACAGCCTGACAGCCACATCAC | 1510 | 1530 | 1550 | 1471 |
| 472 | C L S L A K L P R S P A D S L T A T S L | | | | 491 |

FIG. 1D

MATCH WITH FIG. 1D

| | | | | | |
|------|---|------|------|------|------|
| 1472 | TTTACCTGGCTATGCTGGAGTAACTCAGAGCAGGACTGCCTCACACACTCTCTCCACGA | 1570 | 1590 | 1610 | 1531 |
| 492 | Y L A M S G V T Q S R T A S H T L S T R | | | | 511 |
| 1532 | GGAGCAACAAGGAAGATAGTGGGAGGCAGAGAGATGATATTCTAATGGAGAGCCTTCCA | 1630 | 1650 | 1670 | 1591 |
| 512 | S N K E D S G R Q R D D I L M E K P S R | | | | 531 |
| 1592 | GGCCTATGGAATCTAACCAGACACTGAAGGATGACAAGGAGAACTGAGGATGTTCTCT | 1690 | 1710 | 1730 | 1651 |
| 532 | P M E S N P D T E G | | | | 541 |
| 1652 | GAATGGACATGTGTGGCTGACTTTTCATGGGCTGGTCCAATGGCTGTTGTGTGAGAGGGC | 1750 | 1770 | 1790 | 1711 |
| 1712 | TTGGCTGATACCTCCTATGCTTGAGCACAAAGGCTGAAAATTCAGTTAAGGTGTTACTTAA | 1810 | 1830 | 1850 | 1771 |
| 1772 | TAATAGTTTTTAGGCTCCCATGAATTGGCTCCTGTAAATACTAACGACATGAAAATGCAAG | 1870 | 1890 | 1910 | 1831 |
| 1832 | TGTC AATGGAGTAGTTTATTACCTTCTATTGGCATCAAGTTTCCCTCTAAATTAATGTAT | 1930 | 1950 | 1970 | 1891 |
| 1892 | GGTATTGGCTCTGTGATTGTTCA | 1990 | | | 1914 |

FIG.1E

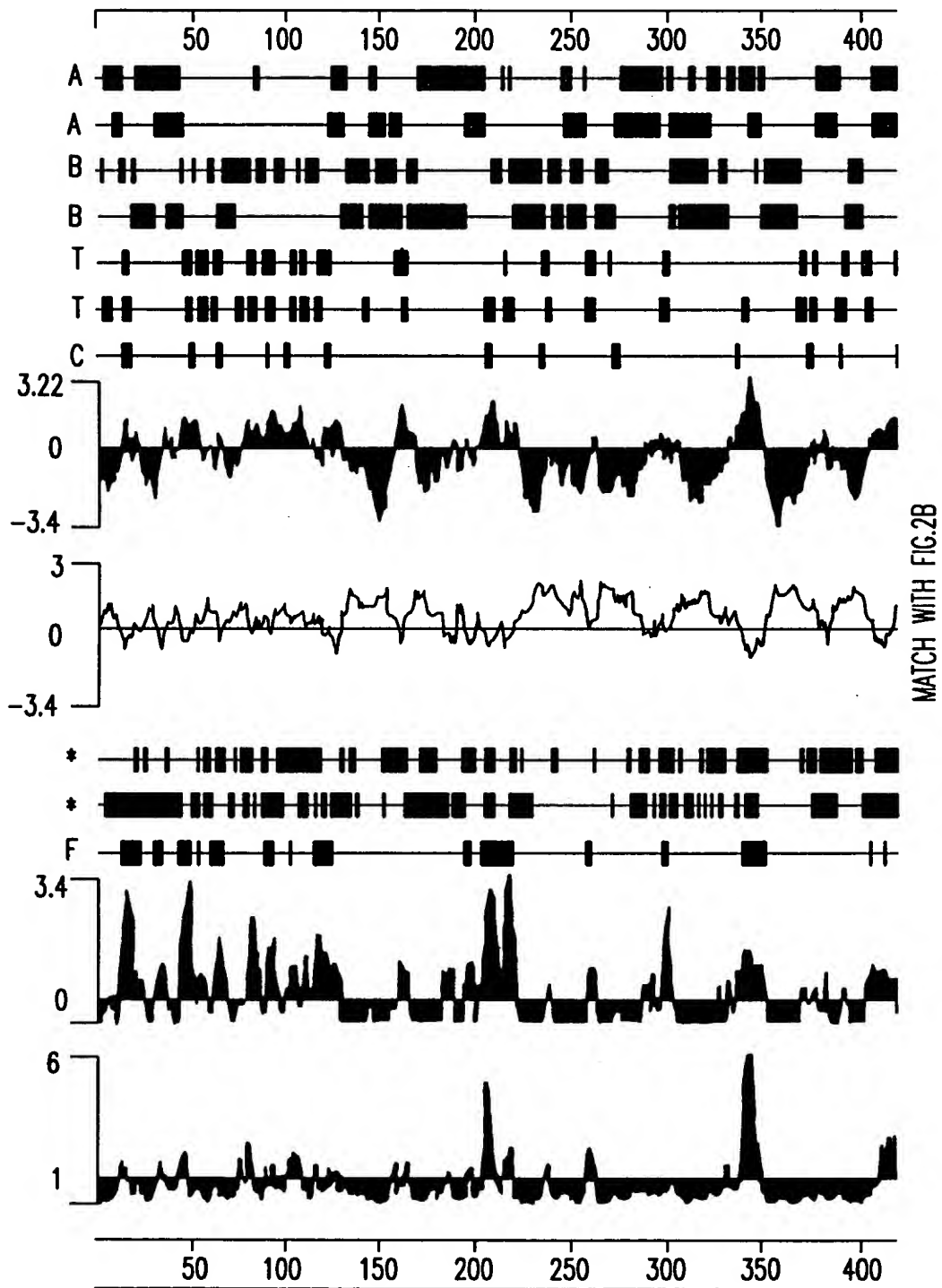


FIG. 2A

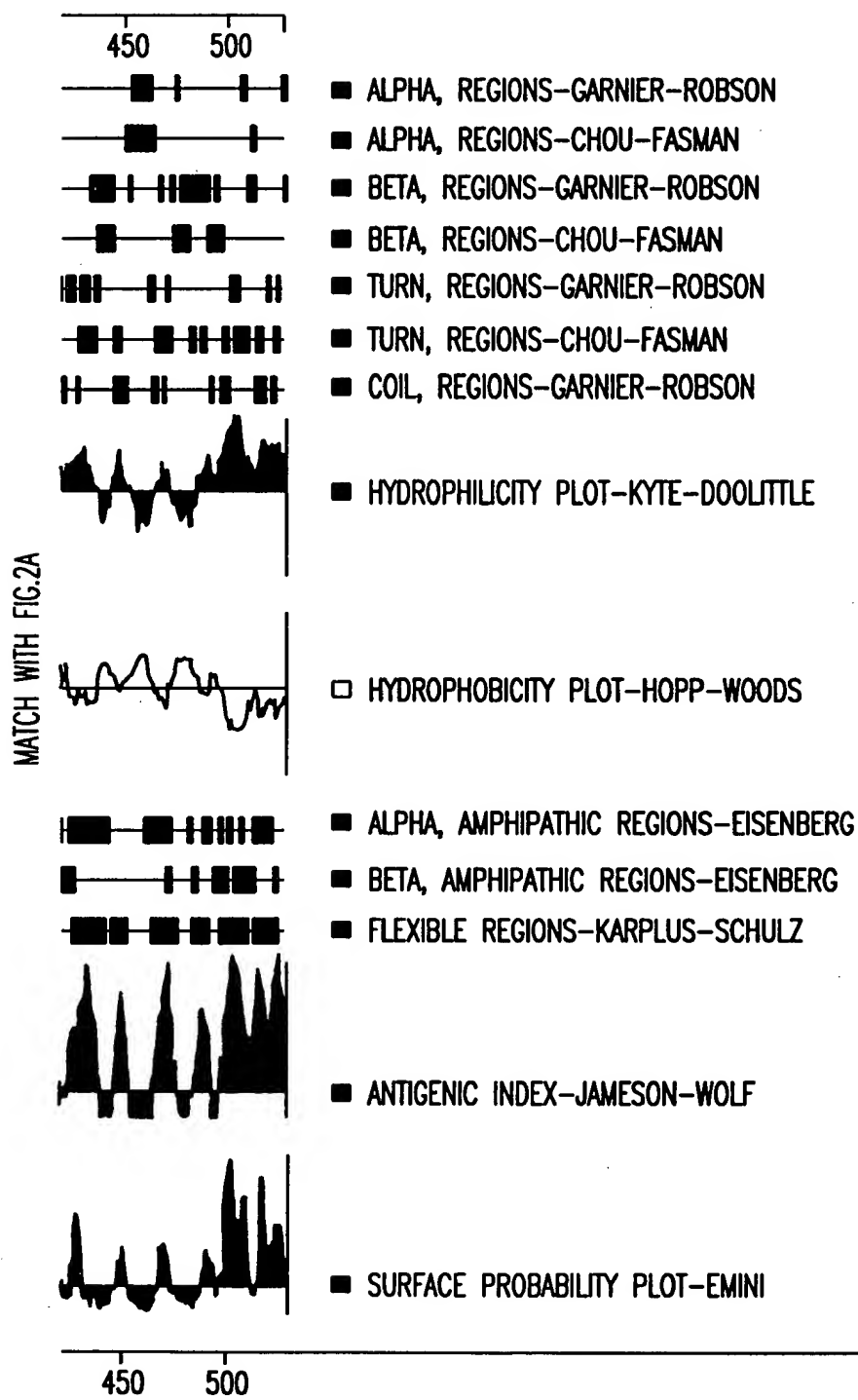


FIG. 2B

| Sequences producing High-scoring Segment Pairs: | | | Reading High Probability | |
|---|--------------------------------------|----|--------------------------|----------|
| | | | Frame Score | P(N) |
| gp M74445 OPOPTH1 | parathyroid hormone receptor [Di... | +3 | 597 | 8.2e-204 |
| pir S A39286 | parathyroid hormone / parathyroid... | +3 | 597 | 2.9e-203 |
| gp L04308 HUMPTH1 | parathyroid hormone receptor [Ho... | +3 | 580 | 6.7e-190 |
| pir S S29610 | parathyroid hormone receptor - h... | +3 | 580 | 6.1e-189 |
| gp M77184 RATPATHYR1 | parathyroid hormone receptor [Ra... | +3 | 576 | 7.7e-188 |
| gp X78936 MMPHRPR1 | parathyroid hormone/parathyroid ... | +3 | 576 | 7.7e-188 |
| pir S A42698 | parathyroid hormone and parathyr... | +3 | 576 | 7.7e-188 |
| gp L34611 MUSPTH061 | parathyroid hormone/parathyroid ... | +3 | 576 | 4.1e-174 |
| gp U11087 HSV1RG91 | vasoactive intestinal peptide 1 ... | +3 | 319 | 1.2e-98 |
| gp M86835 RATVASREC1 | vasoactive intestinal polypeptid... | +3 | 254 | 3.1e-91 |

WARNING: Descriptions of 49 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|M74445|OPOPTH1 parathyroid hormone receptor [Didelphis virginiana]
Length = 585

Plus Strand HSPs:

Score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

Match with FIG. 3B

FIG.3A

Match with FIG. 3 A

Query: 729 IMQDDPQNSIEATSDVKSQYIGCKIAVVMFIYFLATNYYWILVEGLYHLNLIFFAFFSDT 908
 I +++ + E DK+ ++GC++AV +F+YFL TNYWILVEGLYHL+LIF+AFFS+
 Sbjct: 253 ITEELRAFTPEPPADKAGFVGCRAVTVFLYFLTNNYYWILVEGLYHLSLIFMAFFSEK 312

Query: 909 KYLWGFILIGWFPAAFVAWAVARATLADARCWELSAGDIKWYQAPILAAIGLNFILF 1088
 KYLWGF L GWG PA FVA W RATLA+ CW+LS+G+ KWI Q PILAAI +NFILF
 Sbjct: 313 KYLWGF TFGWGLPAVFVAVWTVRATLANTECWDLSSGNKKWIIQVPILAAIVNFILF 372

Query: 1089 LNTVRVLATKIWETNAVGHDTRKQYRKLAKSTLVLVFVGVHYIVFVCLPHS 1244
 +N +RVLATK+ ETNA DTR+QYRKL KSTLVL+ +FGVHYIVF+ P++
 Sbjct: 373 INIIRVLATKLRETNAGRCDTFRQYRKLKSTLVLMPLFGVHYIVFMATPYT 424

Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

Query: 267 EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHHKGVAFRHCNPNGTWDFMHSLNKTW 446
 +G C PEWD ++CWP G GK+ AVPCP YIYDFNHHKG A+R C+ NG+W+ + N+TW
 Sbjct: 102 DGFCLPEWDNIVCWPAGVPGKVAVPCPDYIYDFNHHKGRAYRRCDNSGSEWELVPCNNRTW 161

Query: 447 ANYSDCLRFL 476
 ANYS+C++FL
 Sbjct: 162 ANYSECVKFL 171

Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

Query: 498 KQEFCERLVVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFV 677
 ++E +RL ++YTVGYSIS GSL VA+LI+GYFRRLHCTRNYIHMHLFVSFMLRA SIF+
 Match with FIG. 3 C

FIG. 3B

MATCH WITH FIG. 3B

Sbjct: 177 EREVFDRLGMIYTVGYSSISGLSLTVAVLILGYFRRLLHCTRNYIHMHLFVSFMLRAVSIFI 236

Query: 678 KDRVVHAHIGVKELESIMQD 740

KD V+++ + E+E + ++

Sbjct: 237 KDAVLYSGVSTDEIERITEEE 257

Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

Query: 1248 TGLGWEIRMHCELFNFNSFQGFVSIICYCNGEVQAEVKKMWSRWNLSDWKRTPPCGS 1424

+G+ W++++MH E+ FNSFQGFV+IYC+CNGEVQAE+KK WSRW L++D+KR GS

Sbjct: 427 SGILWQVMHYEMLFNSFQGFVAIIYCFNCNGEVQAEIKKSWSRWTLALDFKRKARSGS 485

Score = 72 (33.1 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

Query: 159 AQLSDGTITIEEQIVLVKAKVQCELNITAQLQEGE 269

A +D+D IT EEQI+L+ A+ QCE + L+ E

Sbjct: 24 ALVDADDVITKEEQIILLRNAQAQCEQLKEVLRVPE 60

Score = 39 (17.9 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

Query: 1508 ISGKAAKIASRQPDSHITLPGYV 1576

+S + A A + H LPGYV

Sbjct: 512 LSPRLAPGAGASANGHHQLPGYV 534

FIG. 3C